

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.  
Goli, Surya K.

(ii) TITLE OF THE INVENTION: NOVEL HUMAN MEMBRANE PROTEIN

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
- (B) STREET: 3174 Porter Drive
- (C) CITY: Palo Alto
- (D) STATE: CA
- (E) COUNTRY: USA
- (F) ZIP: 94304

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Diskette
- (B) COMPUTER: IBM Compatible
- (C) OPERATING SYSTEM: DOS
- (D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: To Be Assigned
- (B) FILING DATE: Herewith
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Billings, Lucy J.
- (B) REGISTRATION NUMBER: 36,749
- (C) REFERENCE/DOCKET NUMBER: PF-0181 US

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415-855-0555
- (B) TELEFAX: 415-845-4166
- (C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 356 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Leu Ala Arg Ala Aia Arg Gly His Trp Gly Pro Phe Ala Glu Gly  
 1               5               10               15  
 Leu Ser Thr Gly Phe Trp Pro Arg Ser Gly Arg Ala Ser Ser Gly Leu  
 20              25              30  
 Pro Arg Asn Thr Val Val Leu Phe Val Pro Gln Gln Glu Ala Trp Val  
 35              40              45  
 Val Glu Arg Met Gly Arg Phe His Arg Ile Leu Glu Pro Gly Leu Asn  
 50              55              60  
 Ile Leu Ile Pro Val Leu Asp Arg Ile Arg Tyr Val Gln Ser Leu Lys  
 65              70              75              80  
 Glu Ile Val Ile Asn Val Pro Glu Gln Ser Ala Val Thr Leu Asp Asn  
 85              90              95  
 Val Thr Leu Gln Ile Asp Gly Val Leu Tyr Leu Arg Ile Met Asp Pro  
 100             105             110  
 Tyr Lys Ala Ser Tyr Gly Val Glu Asp Pro Glu Tyr Ala Val Thr Gln  
 115             120             125  
 Leu Ala Gln Thr Thr Met Arg Ser Glu Leu Gly Lys Leu Ser Xaa Asp  
 130             135             140  
 Lys Val Phe Arg Glu Arg Glu Ser Leu Asn Ala Ser Ile Val Asp Ala  
 145             150             155             160  
 Ile Asn Gln Ala Ala Asp Cys Trp Gly Ile Arg Cys Leu Arg Tyr Glu  
 165             170             175  
 Ile Lys Asp Ile His Val Pro Pro Arg Val Lys Glu Ser Met Gln Met  
 180             185             190  
 Gln Val Glu Ala Glu Arg Arg Lys Arg Ala Thr Val Leu Glu Ser Glu  
 195             200             205  
 Gly Thr Arg Glu Ser Ala Ile Asn Val Ala Glu Gly Lys Lys Gln Ala  
 210             215             220  
 Gln Ile Leu Ala Ser Glu Ala Glu Lys Ala Glu Gln Ile Asn Gln Ala  
 225             230             235             240  
 Ala Gly Glu Ala Ser Ala Val Leu Ala Lys Ala Lys Ala Lys Ala Glu  
 245             250             255  
 Ala Ile Arg Ile Leu Ala Ala Leu Thr Gln His Asn Gly Asp Ala  
 260             265             270  
 Ala Ala Ser Leu Thr Val Ala Glu Gln Tyr Val Ser Ala Phe Ser Lys  
 275             280             285  
 Leu Ala Lys Asp Ser Asn Thr Ile Leu Leu Pro Ser Asn Pro Gly Asp  
 290             295             300  
 Val Thr Ser Met Val Ala Gln Ala Met Gly Val Tyr Gly Ala Leu Thr  
 305             310             315             320  
 Lys Ala Pro Val Pro Gly Thr Pro Asp Ser Leu Ser Ser Gly Ser Ser  
 325             330             335  
 Arg Asp Val Gln Gly Thr Asp Ala Ser Xaa Asp Glu Glu Leu Asp Arg  
 340             345             350  
 Val Lys Met Ser  
 355

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1188 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
- (A) LIBRARY: Consensus
- (B) CLONE: Consensus

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCTTCTGGG	AGCNACCGCT	CCGCTCGTCT	CGTTGGTTCG	GGAGGTCGCT	GCGGCGGTGG	60
GAAATGCTGG	CGCGCGCGC	GCGGGGGCAC	TGGGGCCCTT	TTGCTGAGGG	GCTCTCTACT	120
GGCTTCTGGC	CGCGCTCCGG	CCGCGCCCTCC	TCTGGATTGC	CCC GAAACAC	C GTGGTACTG	180
TTCGTGCCGC	AGCAGGAGGC	CTGGGTGGTG	GAGCGAATGG	GCCGATTCCA	CCGGATCCTG	240
GAGCCTGGTT	TGAACATCCT	CATCCCTGTG	TTAGACCAGA	TCCGATATGT	GCAGAGTCTC	300
AAGGAAATTG	TCATCAACGT	GCCTGAGCAG	TCGGCTGTGA	CTCTCGACAA	TGTAACTCTG	360
CAAATCGATG	GAGTCCTTTA	CCTGCCATC	ATGGACCCCTT	ACAAGGCAAG	CTACGGTGTG	420
GAGGACCCCTG	AGTATGCCGT	CACCCAGCTA	GCTCAAACAA	CCATGAGATC	AGAGCTCGGC	480
AAAATCTCTN	TGGACAAAGT	CTTCCGGGAA	CGGGAGTC	TGAATGCCAG	CATTGTGGAT	540
GCCATCAACC	AAGCTGCTGA	CTGCTGGGGT	ATCCGCTGCC	TNCGTTATGA	GATCAAGGAT	600
ATCCATGTGC	CACCCCGGGT	GAAAGAGTCT	ATGCAGATGC	AGGTGGAGGC	AGAGCGCGG	660
AAACGGGCCA	CAGTCTAGA	GTCTGAGGGG	ACCCGAGAGT	CGGCCATCAA	TGTGGCAGAA	720
GGGAAGAAC	AGGCCAGAT	CCTGGCCTCC	GAAGCAGAAA	AGGCTGAACA	GATAAATCAG	780
GCAGCAGGAG	AGGCCAGTGC	AGTTCTGGCG	AAGGCCAAGG	CTAAAGCTGA	AGCTTATTGCA	840
ATCCTGGCTG	CAGCTCTGAC	ACAACATAAT	GGAGATGCAG	CAGCTTCACT	GACTGTGCC	900
GAGCAGTATG	TCAGCGCGTT	CTCCAAACTG	GCCAAGGACT	CCAACACTAT	CCTACTGCC	960
TCCAACCCTG	GCGATGTCAC	CAGCATGGTG	GCTCAGGCCA	TGGGTGTATA	TGGAGCCCTC	1020
ACCAAAGCCC	CAGTGCCAGG	GAETCCAGAC	TCACTCTCCA	GTGGGAGCAG	CAGAGATGTC	1080
CAGGGTACAG	ATGCAAGTNT	TGATGAGGAA	CTTGATCGAG	TCAAGATGAG	TTAGTGGAGC	1140
TGGGCTTNGC	CAGGGAGTCT	GGGGACAAGG	AAGCAGATT	TCCTGATT		1188

## (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 288 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
 (A) LIBRARY: Genbank  
 (B) CLONE: 31069

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ala	Glu	Lys	Arg	His	Thr	Arg	Asp	Ser	Glu	Ala	Gln	Arg	Leu	Pro
1		5							10			15			
Asp	Ser	Phe	Lys	Asp	Ser	Pro	Ser	Lys	Gly	Leu	Gly	Pro	Cys	Gly	Trp
								20	25			30			
Ile	Leu	Val	Ala	Phe	Ser	Phe	Leu	Phe	Thr	Val	Ile	Thr	Phe	Pro	Ile
								35	40			45			
Ser	Ile	Trp	Met	Cys	Ile	Lys	Ile	Ile	Lys	Glu	Tyr	Glu	Arg	Ala	Ile
			50		55				60						
Ile	Phe	Arg	Leu	Gly	Arg	Ile	Leu	Gln	Gly	Gly	Ala	Lys	Gly	Pro	Gly
			65		70			75			80				
Leu	Phe	Phe	Ile	Leu	Pro	Cys	Thr	Asp	Ser	Phe	Ile	Lys	Val	Asp	Met
								85		90			95		
Arg	Thr	Ile	Ser	Phe	Asp	Ile	Pro	Pro	Gln	Glu	Ile	Leu	Thr	Lys	Asp
								100		105		110			
Ser	Val	Thr	Ile	Ser	Val	Asp	Gly	Val	Val	Tyr	Tyr	Arg	Val	Gln	Asn
			115					120			125				
Ala	Thr	Leu	Ala	Val	Ala	Asn	Ile	Thr	Asn	Ala	Asp	Ser	Ala	Thr	Arg
								130		135		140			
Leu	Leu	Ala	Gln	Thr	Leu	Arg	Asn	Val	Leu	Gly	Thr	Lys	Asn	Leu	
	145							145		150		155		160	
Ser	Gln	Ile	Leu	Ser	Asp	Arg	Glu	Glu	Ile	Ala	His	Asn	Met	Gln	Ser
								165		170			175		
Thr	Leu	Asp	Asp	Ala	Thr	Asp	Ala	Trp	Gly	Ile	Lys	Val	Glu	Arg	Val
								180		185		190			
Glu	Ile	Lys	Asp	Val	Lys	Leu	Pro	Val	Gln	Leu	Gln	Arg	Ala	Met	Ala
								195		200		205			

Ala	Glu	Ala	Glu	Ala	Ser	Arg	Glu	Ala	Arg	Ala	Lys	Val	Ile	Ala	Ala
210					215						220				
Glu	Gly	Glu	Met	Asn	Ala	Ser	Arg	Ala	Leu	Lys	Glu	Ala	Ser	Met	Val
225					230					235					240
Ile	Thr	Glu	Ser	Pro	Ala	Ala	Leu	Gln	Leu	Arg	Tyr	Leu	Gln	Thr	Leu
						245				250					255
Thr	Thr	Ile	Ala	Ala	Glu	Lys	Asn	Ser	Thr	Ile	Val	Phe	Pro	Leu	Pro
					260				265			270			
Ile	Asp	Met	Leu	Gln	Gly	Ile	Ile	Gly	Ala	Lys	His	Ser	His	Leu	Gly
					275				280			285			

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1065452

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Asn	Leu	Lys	Thr	Cys	Ser	Leu	Ser	Thr	His	Ser	Phe	Leu	Gln	Lys
1							5		10					15	
Lys	Asn	Glu	Lys	His	Asp	Gly	Asn	Pro	Glu	His	Tyr	Asp	Thr	Gly	Leu
							20		25					30	
Gly	Phe	Cys	Gly	Trp	Phe	Leu	Met	Gly	Leu	Ser	Trp	Ile	Met	Val	Ile
						35		40				45			
Ser	Thr	Phe	Pro	Val	Ser	Ile	Tyr	Phe	Cys	Met	Lys	Val	Val	Gln	Glu
						50		55			60				
Tyr	Glu	Arg	Ala	Val	Ile	Phe	Arg	Leu	Gly	Arg	Leu	Ile	Gly	Gly	
						65		70			75			80	
Ala	Lys	Gly	Pro	Gly	Ile	Phe	Phe	Val	Leu	Pro	Cys	Ile	Glu	Ser	Tyr
						85		90					95		
Thr	Lys	Val	Asp	Leu	Arg	Thr	Val	Ser	Phe	Ser	Val	Pro	Pro	Gln	Glu
						100		105					110		
Ile	Leu	Thr	Lys	Asp	Ser	Val	Thr	Thr	Ser	Val	Asp	Ala	Val	Ile	Tyr
						115		120				125			
Tyr	Arg	Ile	Ser	Asn	Ala	Thr	Val	Ser	Val	Ala	Asn	Val	Glu	Asn	Ala
						130		135			140				
His	His	Ser	Thr	Arg	Leu	Leu	Ala	Gln	Thr	Leu	Arg	Asn	Met	Leu	
						145		150			155			160	
Gly	Thr	Arg	Ser	Leu	Ser	Glu	Ile	Leu	Ser	Asp	Arg	Glu	Thr	Leu	Ala
						165		170				175			
Ala	Ser	Met	Gln	Thr	Ile	Leu	Asp	Glu	Ala	Thr	Glu	Ser	Trp	Gly	Ile
						180		185			190				
Lys	Val	Glu	Arg	Val	Glu	Ile	Lys	Asp	Val	Arg	Leu	Pro	Ile	Gln	Leu
						195		200			205				
Gln	Arg	Ala	Met	Ala	Ala	Glu	Ala	Glu	Ala	Thr	Arg	Glu	Ala	Arg	Ala
						210		215			220				
Lys	Val	Ile	Ala	Ala	Glu	Gly	Glu	Gln	Lys	Ala	Ser	Arg	Ala	Leu	Arg
						225		230			235			240	
Asp	Ala	Ala	Ser	Val	Ile	Ala	Gln	Ser	Pro	Ala	Ala	Leu	Gln	Leu	Arg
						245		250				255			
Tyr	Leu	Gln	Thr	Leu	Asn	Ser	Val	Ala	Arg	Glu	Lys	Phe	Asp	Asp	His
						260		265			270				
Leu	Pro	Thr	Ser	Asp	Gly	Ile	Ser								
						275		280							

## (2) INFORMATION FOR SEQ ID NO:5:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1353669

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Glu	Tyr	Gly	Met	Pro	Glu	Gly	Ser	Tyr	Asp	Ser	Val	Phe	Thr	Tyr
1	5					10						15			
Ala	Pro	Tyr	Asn	Asp	Leu	Asp	Lys	Met	Gly	Tyr	Met	Gly	Pro	Ala	Arg
		20				25						30			
Gln	Gly	Met	Met	Leu	Gly	Asn	Lys	Tyr	Gly	Asn	Phe	Thr	Tyr	Thr	Arg
		35				40						45			
Asp	Tyr	Gly	Val	Asn	Met	Glu	Asp	Asp	Ile	Lys	Pro	Leu	Ser	Ala	Ile
	50				55						60				
Glu	Leu	Leu	Ile	Phe	Cys	Val	Ser	Phe	Leu	Phe	Val	Val	Met	Thr	Met
	65				70					75			80		
Pro	Leu	Ser	Leu	Leu	Phe	Ala	Leu	Lys	Phe	Ile	Ser	Thr	Ser	Glu	Lys
		85				90						95			
Leu	Val	Val	Leu	Arg	Leu	Gly	Arg	Ala	Gln	Lys	Thr	Arg	Gly	Pro	Gly
	100				105						110				
Ile	Thr	Leu	Val	Ile	Pro	Cys	Ile	Asp	Thr	Thr	His	Lys	Val	Thr	Met
	115				120						125				
Ser	Ile	Thr	Ala	Phe	Asn	Val	Pro	Pro	Leu	Gln	Ile	Ile	Thr	Thr	Asp
	130				135						140				
Arg	Gly	Leu	Val	Glu	Leu	Gly	Ala	Thr	Val	Phe	Leu	Lys	Ile	Arg	Asp
	145				150					155			160		
Pro	Ile	Ala	Ala	Val	Cys	Gly	Val	Gln	Asp	Arg	Asn	Ala	Ser	Val	Arg
		165				170						175			
Thr	Leu	Ala	Asn	Thr	Met	Leu	Tyr	Arg	Tyr	Ile	Ser	Lys	Lys	Arg	Ile
		180				185						190			
Cys	Asp	Val	Thr	Ser	Ser	Gln	Asp	Arg	Arg	Ile	Ile	Ser	Ala	Asn	Leu
		195				200						205			
Lys	Asp	Glu	Leu	Gly	Ser	Phe	Thr	Cys	Gln	Phe	Gly	Val	Glu	Ile	Thr
	210					215					220				
Asp	Val	Glu	Ile	Ser	Asp	Val	Lys	Ile	Val	Lys	Glu	Gly	Glu	Asn	Met
	225					230				235			240		
Gly	Met	Ser	Ala	Leu	Ser	Ser	Val	Ala	Lys	Ser	Asp	Ala	Gly	Gln	Gln
		245					250					255			
Leu	Trp	Gln	Val	Ile	Gly	Pro	Val	Phe	Glu	Asp	Phe	Ala	Lys	Glu	Cys
		260					265					270			
Ala	Ala	Glu	Glu	Lys	Ala	Lys	Glu	Asn	Ala	Pro	Leu	Val	Asp	Leu	Ser
		275					280					285			
Asp	Val	Pro	Ser	Thr	Ser	Ala	Ala	Gly	Thr	Ser	Thr	Asp	Thr	Pro	Asn
	290					295					300				
Ile	Pro	Ser	Ile	Asp	Ile	Asp	His	Leu	Ile	Ser	Val	Ala	Ser	Leu	Ala
	305					310				315			320		
Met	Asp	Glu	His	Leu	Val	Arg	Leu	Ile	Gly	Arg	Val	Phe	Gln	Ile	Asn
			325				330					335			
Cys	Lys	Asp	Ile	Glu	Pro	Ile	Cys	Ile	Asp	Leu	Lys	His	Gly	Ser	Gly
			340				345					350			
Ser	Ala	Tyr	Lys	Gly	Thr	Ser	Leu	Asn	Pro	Asp	Val	Val	Phe	Glu	Thr
		355					360					365			
Ser	Leu	Glu	Val	Phe	Gly	Lys	Ile	Leu	Thr	Lys	Glu	Val	Ser	Pro	Val

370	375	380
Thr Val Tyr Met Asn Gly Asn Leu Lys Val Lys Gly Ser Ile Gln Asp		
385	390	395
Ala Met Gln Leu Lys His Leu Val Glu Arg Met Ser Asp Trp Leu		
405	410	415

## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Owl
- (B) CLONE: 79701

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Gly Ala Val Ala Gly Leu Val Phe Leu Ala Val Leu Val Ile  
 1               5               10               15  
 Phe Ala Ile Ile Val Val Ala Lys Ser Val Ala Leu Ile Pro Gln Ala  
 20               25               30  
 Glu Ala Ala Val Ile Glu Arg Leu Gly Arg Tyr Ser Arg Thr Val Ser  
 35               40               45  
 Gly Gln Leu Thr Leu Leu Val Pro Phe Ile Asp Arg Val Arg Ala Arg  
 50               55               60  
 Val Asp Leu Arg Glu Arg Val Val Ser Phe Pro Pro Gln Pro Val Ile  
 65               70               75               80  
 Thr Glu Asp Asn Leu Thr Leu Asn Ile Asp Thr Val Val Tyr Phe Gln  
 85               90               95  
 Val Thr Val Pro Gln Ala Ala Val Tyr Glu Ile Ser Asn Tyr Ile Val  
 100              105              110  
 Gly Val Glu Gln Leu Thr Thr Leu Arg Asn Val Val Gly Gly  
 115              120              125  
 Met Thr Leu Glu Gln Thr Leu Thr Ser Arg Asp Gln Ile Asn Ala Gln  
 130              135              140  
 Leu Arg Gly Val Leu Asp Glu Ala Thr Gly Arg Trp Gly Leu Arg Val  
 145              150              155              160  
 Ala Arg Val Glu Leu Arg Ser Ile Asp Pro Pro Pro Ser Ile Gln Ala  
 165              170              175  
 Ser Met Glu Lys Gln Met Lys Ala Asp Arg Glu Lys Arg Ala Met Ile  
 180              185              190  
 Leu Thr Ala Glu Gly Thr Arg Glu Ala Ala Ile Lys Gln Ala Glu Gly  
 195              200              205  
 Gln Lys Gln Ala Gln Ile Leu Ala Ala Glu Gly Ala Lys Gln Ala Ala  
 210              215              220  
 Ile Leu Ala Ala Glu Ala Asp Arg Gln Ser Arg Met Leu Arg Ala Gln  
 225              230              235              240  
 Gly Glu Arg Ala Ala Ala Tyr Leu Gln Ala Gln Gly Gln Ala Lys Ala  
 245              250              255  
 Ile Glu Lys Thr Phe Ala Ala Ile Lys Ala Gly Arg Pro Thr Pro Glu  
 260              265              270  
 Met Leu Ala Tyr Gln Tyr Leu Gln Thr Leu Pro Glu Met Ala Arg Gly  
 275              280              285  
 Asp Ala Asn Lys Val Trp Val Val Pro Ser Asp Phe Asn Ala Ala Leu  
 290              295              300  
 Gln Gly Phe Thr Arg Leu Leu Gly Lys Pro Gly Glu Asp Gly Val Phe  
 305              310              315              320  
 Arg Phe Glu Pro Ser Pro Val Glu Asp Gln Pro Lys His Ala Ala Asp

325		330		335
Gly Asp Asp Ala Glu Val Ala Gly Trp Phe Ser Thr Asp Thr Asp Pro				
340		345		350
Ser Ile Ala Arg Ala Val Ala Thr Ala Glu Ala Ile Ala Arg Lys Pro				
355		360		365
Val Glu Gly Ser Leu Gly Thr Pro Pro Arg Leu Thr Gln				
370		375		380

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: 1591514

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Lys Val Asn Asp Met Phe Trp Phe Trp Leu Ile Leu Gly Ile Ile				
1	5	10	15	
Ala Leu Phe Ile Ile Val Lys Ala Ile Val Ile Val Asn Gln Tyr Glu				
20	25	30		
Gly Gly Leu Ile Phe Arg Leu Gly Arg Val Ile Gly Lys Leu Lys Pro				
35	40	45		
Gly Ile Asn Ile Ile Ile Pro Phe Leu Asp Val Pro Val Lys Val Asp				
50	55	60		
Met Arg Thr Arg Val Thr Asp Ile Pro Pro Gln Glu Met Ile Thr Lys				
65	70	75	80	
Asp Asn Ala Val Val Lys Val Asp Ala Val Val Tyr Tyr Arg Val Ile				
85	90	95		
Asp Val Glu Lys Ala Ile Leu Glu Val Glu Asp Tyr Glu Tyr Ala Ile				
100	105	110		
Ile Asn Leu Ala Gln Thr Thr Leu Arg Ala Ile Ile Gly Ser Met Glu				
115	120	125		
Leu Asp Glu Val Leu Asn Lys Arg Glu Tyr Ile Asn Ser Lys Leu Leu				
130	135	140		
Glu Ile Leu Asp Arg Glu Thr Asp Ala Trp Gly Val Arg Ile Glu Lys				
145	150	155	160	
Val Glu Val Lys Glu Ile Asp Pro Pro Glu Asp Ile Lys Asn Ala Met				
165	170	175		
Ala Gln Gln Met Lys Ala Glu Arg Leu Lys Arg Ala Ala Ile Leu Glu				
180	185	190		
Ala Glu Gly Glu Lys Pro Glu				
195				